Bureau of Rural Science Department of Primary Industry

LIVESTOCK DISEASE SURVEYS

A FIELD MANUAL FOR VETERINARIANS

R.M. Cannon and R.T. Roe

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INTRODUCTION

The Epidemiology Branch of the Bureau is frequently asked questions such as 'How many animals do we need to test to determine whether a certain disease is present in a herd or flock?' or 'How should we carry out a survey to find the prevalence of a disease in a State?'. This manual is an attempt to make the answers to these and similar questions available to field veterinarians in an easy-to-follow form.

The material included in this manual is not original. All the principles and concepts discussed are covered in texts on sampling theory or statistical methods. However, it is not always easy for a veterinarian to put his hand on an appropriate book when required and the treatment given in such books is often in unfamiliar terms. We have attempted to present the same material in the context of the types of questions we are frequently asked.

Section 1 deals with questions that must be answered when attempting to detect the presence of a disease, while Section 2 deals with estimating the level of occurrence of a disease present in a population. Section 3 considers sampling methodology and Section 4 discusses some commonly used (and misused) terms and concepts. Tables are included to provide the answers to the problems discussed in Sections 1 and 2.

For those who wish to obtain further detail of the principles and mathematical theory behind sampling techniques, a series of Appendices and a list of further reading are included.

1. SURVEYS TO DETECT THE PRESENCE OF DISEASE

1.1 Proving that a Disease is Not Present

Field veterinarians are frequently asked to certify the freedom of animal groups or populations from certain diseases. What testing needs to be undertaken to be able to give such a certification?

In some cases those wanting the certification will prescribe tests that must be conducted on all animals in the group. In this case no sampling considerations arise - all must be tested.

In other cases the veterinarian may be asked to certify as to the disease status of the property of origin of the animals moving interstate or overseas. In most cases the certification required will be that, to the best of the certifying officer's knowledge and belief, there has been no evidence of the disease in question on the property of origin of the stock during the previous 12 months. In such a case, so long as the certifying officer can satisfy himself that the animals in question have not been off the property in the previous 12 months, the certification could be given on the basis of records and knowledge of the disease history of the property.

However, in some cases the veterinarian may be asked to certify that the property of origin is <u>free</u> of a certain disease. In the absence of records of whole herd tests for the specified diseases, this would require the testing of at least a sample of the animals on the property. The sample tested should be of sufficient size to give 95% confidence that the disease is not present at a prevalence that is substantially below the prevalence expected on a diseased property. This question will be answered in section 1.2.

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To prove that a disease is not present in a population, particularly if the disease could be present at a low level, requires the testing of <u>all</u> susceptible individuals in the population.

1.2 Detecting the Presence of a Disease

The size of the sample which needs to be tested to determine whether a disease is present in a particular population depends on:

- a) the size of the animal population in question
- b) if the disease is present, the likely prevalence
- c) the reliability required of the conclusions.

a) Size of the population to be sampled

If the sample makes up a significant proportion of the total population, the progressive sampling of negative animals from the population increases the probability that the next animal sampled will be positive. This effect is insignificant if the population to be surveyed is very large compared to the sample size.

b) The expected level of occurrence of the condition, if present

In most cases if a disease is present in a herd or flock we can expect some proportion, rather than a single animal, to be infected. An estimate of the likely level of occurrence can be made from the epidemiology of the disease and results of surveys in other herds or flocks. The higher the prevalence, the smaller the sample size that is required to detect an infected animal.

Thus a sample size can be chosen such that, if the sample is negative, it may be concluded that it is unlikely that any animal in the herd or flock has the disease.

c) Reliability of the conclusions drawn

By adopting a sampling procedure we are accepting, for the sake of economy, that we will not be able to make an absolute statement based on our findings. The larger the sample, the greater the confidence that can be placed in the results. The sample size can be chosen to give the confidence level desired.

The confidence levels that have generally been used in disease surveys are 95% or, occasionally, \$\infty\$99%. For example, suppose that the sample size has been chosen to give us 95% confidence of detecting antibodies if they are present in 10% of the herd. This means that, on average, 5 out of 100 herds with a 10% prevalence would not be detected as infected by our survey. However, very few herds with an antibody prevalence greater than 10% would not be detected by the survey, while the error rate for herds with a prevalence less than 10% would be greater than 5 in 100. Thus, if we expect infected herds to contain 20% to 50% positive animals, the testing of a sample that gave 95% confidence of detecting a 10% level of infected animals would detect most infected herds.

Table 1 gives the sample size required to detect various minimum levels of infection in different sized herds or flocks at one of three confidence levels.

Tables 2 and 3 look at this information in two other ways. Table 2 illustrates the effect that different proportions of sampling have on the chances of detecting a positive in populations with a small number of positives, while Table 3 shows the effect of sample size on the probability of detecting a positive in a population with a specified proportion of positives.

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ortion of the total animals from the animal sampled will e population to be Disease monitoring poses a different problem. Consider, as an example, abattoir surveillance for brucellosis. We know the proportion of the herd that has been tested at slaughter. If all of these were negative, we wish to know if this is sufficient to say that the herd is negative, and so avoid doing a whole herd test.

The question to be answered is thus the converse of the one faced in Section 1.1. Rather than wanting to determine the sample size required for a given level of confidence of detecting disease, we want an indication of the level of disease that may be present given that our surveillance sample is negative. Table 1 can also be used to answer this question and gives the upper limit for the number of positives that could be present in the population given that none were detected in the surveillance sample. Again Tables 2 and 3 provide an alternate way of looking at the problem.

A Special Word About Abattoir Surveillance for Disease

Tables 1 to 3 assume that a random sample is tested. However, slaughter animals are not a true random sample of the population. Animals sent for slaughter are those judged by their owners to be in a suitable condition. Most of these animals will be free from any clinical disease. Slaughter animals will also be unrepresentative of the age structure and sex ratio of the population from which they are derived. Individuals with a poor performance in such things as reproduction or milk production are likely to be over-represented in slaughter animals.

Care must therefore be exercised in drawing inferences about the prevalence of disease in a population based on abattoir survey results. While information on the prevalence of conditions that do not affect the preparation of animals for slaughter (and do not affect the likelihood of an animal being culled) may be obtained from carefully planned abattoir surveys, thought needs to be given to the possible biases in this method before commencing a survey.

On the other hand, trace-back from abattoir surveillance does provide a cost effective method of identifying diseased herds and flocks. Abattoir surveillance data can also be cumulated from one period to the next - thereby building up a record on the herds or flocks of origin. In this respect the tables are not strictly correct since the animals in the herd or flock for which the percentage monitored is calculated is a changing population with replacements being bred or introduced. The effect of this, however, will generally be to increase the probability of detecting disease above the levels given in Table 1.

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2. SURVEYS TO MEASURE THE PREVALENCE OF DISEASE

2.1 Establishing the Level of Occurrence of a Disease

Estimation of the prevalence of a disease involves the same sampling theory as detecting the presence of disease. In fact, surveying for the presence of a disease is a special application of the procedure followed in estimating the prevalence of disease in a population.

Again the sample size required will depend on the level of the disease in the population, the confidence level desired and the size of the population.

However, the question usually posed in relation to surveying to determine the prevalence of disease is, 'Having tested a random sample of animals from a population of known size and found a certain proportion of these to be positive, what does this mean about the level of disease in the population?'.

Table 4 gives an estimate of the number of animals that need to be tested if it is desired to estimate, with a specified confidence level, the proportion within the population that have the disease.

Table 5 gives the possible range for the disease prevalence in a population, for three different confidence levels, that can be deduced from the findings of a survey test of a given number of animals. If more precision is required, then it is necessary to test additional randomly selected animals from the same population until the required precision is obtained.

3. SAMPLING METHODS

In the previous sections concerning the size of the sample required for various purposes, it has been assumed that the sample to be surveyed would be selected at random. Without proper randomisation, we cannot validly extrapolate from the sample we have surveyed to make inferences about the population it is supposed to represent.

Random does not mean haphazard. It has been demonstrated repeatedly that it is virtually impossible to prevent the introduction of some form of bias, either consciously or sub-consciously, in selecting a sample by means other than a randomizing process. To select a proper random sample requires rigorous adherence to a predetermined random selection procedure.

The four common sampling methods are described below. These are often used in various combinations.

3.1 Simple Random Sampling

A simple random sample is a sample selected such that each animal in the population being surveyed has an equal opportunity of being included in the sample. The tables included in this booklet for determining sample size etc. are all based on the selection of a simple random sample. If the sample tested is not a simple random sample these tables do not apply and larger samples will be required.

A random sample may be selected by numbering each animal in the population (such as by ear-tag numbers), writing these numbers on slips of paper, mixing them in a hat, and drawing the required number of slips from the hat to identify the members of the sample. A more convenient way of choosing the numbers is to use a table of random numbers such as Table 6.

3.2 Systematic Sampling

In systematic sampling, animals are selected for inclusion in the sample at equal intervals from the (ordered) population. If a sample of 1/n of the population is required, we would start at a randomly selected animal in the first n animals, and thereafter sample every nth animal.

For a systematic sample, the population size need not be known before the survey starts. This is particularly useful when prospectively sampling events such as live births or laboratory accessions. To select a random sample containing 1/n of a population, the size of the population must be known (at least approximately).

Systematic sampling will usually be much easier than random sampling and on occasions may be the only practicable method. However, care must be taken in systematic sampling, if cyclic fluctuations exist in the population, that the sample interval does not coincide with the fluctuation interval.

Systematic sampling is appropriate for quality control testing on production lines.

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The population of a livestock species on any property is normally managed in a number of discrete herds or flocks. Where the sample to be selected is very small in comparison with the total population, it is quite likely that a simple random sample selected from the total population, could, by chance, severely under-represent (or completely exclude) some herds or flocks. A random sample of herds will under-represent animals in large herds, whereas a random sample of animals will under-represent small herds. This can be avoided by stratified sampling, which ensures that each group or unit in the aggregate population is adequately represented.

For example, suppose we wish to sample 58 sheep from a property running 7800 sheep as part of a survey. (A sample of 58 would give 95% confidence of detecting the presence of a condition if present at a prevalence of 5% or greater.) If the 7800 sheep are run in four separate flocks, we should sample from each flock in the same proportion it is to the total population (rounding up to the next whole number in each case).

number in	flock	number sampled
Ewes Maiden ewes	3000 800	58 x 3000 ÷ 7800 = 23
Weaners Wethers	2500 1500	19
e 1 ¹¹ 11 11 11 1 e 1	7800	12 60

If the animals selected from each flock are a random sample of that flock, we then have a stratified random sample, which can be termed a random sample stratified by flock size of the sheep on that property.

3.4 Cluster Sampling

In cluster sampling, groups or clusters of individuals are chosen for testing. The groups may be chosen at random or systematically, but no control is exercised over membership of each group. Cluster sampling is frequently resorted to where no reliable list of all members of the population is available from which a random sample may be selected.

A random sample of farms on which all relevant animals are tested would be a cluster sample in which the animals on each farm constitute a cluster. While such a sample of farms may be easy to select and convenient for field work, care needs to be exercised in drawing inferences about the disease situation in the animal population, as distinct from the population of farms, from the results. The information obtained will be less accurate than if a sample of the same size, drawn systematically or at random from a list of individual animals, is surveyed. This is because disease statistics, particularly for infectious diseases, are in general more variable between herds than within herds.

Cluster sampling may be applicable to some production line sampling programs such as <u>Salmonella</u> testing of meat products.

3.5 <u>Multistage Sampling</u>

Multistage sampling is a term applied to the selection of a sample in two or more stages. An example would be to randomly select a sample of dairy herds in a State and then to select a random sample of heifers from each of these herds for testing.

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4. TERMS AND CONCEPTS

4.1 Prevalence and Incidence

The terms prevalence and incidence are often confused. Frequently the term 'incidence' is used when clearly what is meant is point prevalence.

The point prevalence of a disease is the proportion of a specified population with the disease at a particular point in time. Thus, in most field surveys, it is the point prevalence that is being determined.

On the other hand, the <u>incidence</u> of a disease is the number of new cases of the disease that <u>occurred</u> during a specified period of time. It is a measure of the rapidity with which a disease is occurring or spreading and is usually expressed as a fraction or percentage of the average number of animals in the population during the time period.

Much of the confusion between prevalence and incidence arises because of a third term, period prevalence. Period prevalence is the total number of cases both new and old that have existed at some time during a specified period of time. It is thus a combination of the point prevalence at the beginning of the period and the incidence of new cases during the period. The period prevalence is of limited usefulness in characterising a disease and is most frequently used in describing the pattern of mild, self-limiting diseases.

4.2 Ratios, Proportions and Rates

'Epidemiology is the science of denominators and, as such, is the rational counter-balance of clinical training, which tends to be preoccupied with numerators. The introduction of the denominator was about as important in medical thinking as the invention of the wheel, and equally revolutionary. The denominator is our foundation for rates, and hence for our sense of proportion and priorities. Denominators are dull but indispensible whenever and wherever we try to draw conclusions about distributions, differences, and dividends - fiscally, socially or medically.' (Stewart, 1970).

In epidemiology, as in most scientific disciplines, there is often a certain lack of precision leading to ambiguity in the terminology used. One reason for this may be that workers in one field borrow terms from another field in which they are not specialists. Another reason is semantics; a word may have more than one meaning in common usage or people may use two words as synonyms when, in fact, their meanings are distinct.

The use of the word <u>rate</u> in epidemiology suffers from these disadvantages; it is borrowed from physics and misinterpreted; it has more than one meaning in the English language; and the most common error - it is used inter-changeably with the term <u>proportion</u> because both are incorrectly assumed to be synonyms for <u>ratio</u>.

Ratio is the expression of the relationship between a numerator and denominator where the two are separate and distinct quantities; neither is included in the other. Usually the numerator and denominator are measured in the same units, although this is not essential. For example,

sex ratio = number of males : number of females

foetal death ratio = number of foetal deaths

number of live births

An <u>index</u> is a comparative measure of two characteristics frequently expressed as a ratio. For example, weight-height index is a ratio used as a measure of obesity.

Proportion, like a ratio, is a relative frequency, but in this case the numerator is included in the denominator, i.e. the proportion some group is of the whole population. For example,

proportion of males = number of males number of males + number of females

proportion of foetal deaths = number of foetal deaths number of conceptions

These relative frequencies can be used as an estimate of the probability of an event occurring.

Rate is an expression for the change in one quantity per unit of another quantity, which is frequently time. However, in many biological processes it is not the absolute change per unit time that is of interest, but the relative change per unit of time and per unit of the organism or population undergoing the change - the relative rate. However, since this kind of rate is the most commonly used, the word 'relative' is frequently omitted unless ambiguity would arise from its omission.

Incidence is an example of a rate. Since incidence is the number of new cases in a time period, it is clearly a rate. It does not refer to the population size. We should more properly use relative incidence to refer to the number of new cases per 1000 animals per year. However, by convention we also refer to this as 'incidence', and let the way in which the result is expressed indicate whether we are dealing with a relative rate or not.

Care needs to be taken in selecting the denominator for a relative rate. It is usual to use the mid-period population size rather than the size at the start or end of the period. In a stable situation this may not matter, but, in an epidemic there can be considerable differences between the rates calculated with different denominators. In such cases it may be better to calculate the incidence for shorter periods. Incidence over a short period is generally referred to as the attack rate.

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By contrast, <u>prevalence</u>, which is the number of cases at a given time expressed as a proportion of the total population at that time, is clearly a proportion and not a rate. The term 'prevalence rate' is erroneous.

4.3 Sensitivity and Specificity

Most field surveys will involve the use of diagnostic tests (generally serological) for the disease in question. In deciding on the test procedures to be used in a large scale survey, some compromise in regard to accuracy for the sake of simplicity, cost, and acceptability of the test procedure will frequently have to be made. However, there is little point in conducting a large scale survey involving considerable effort in obtaining data if it is not known what the test results mean in terms of the true disease situation. The inferences that can be drawn about the disease situation depend on the characteristics of the diagnostic test being used. These characteristics can be defined in terms of repeatability, accuracy, sensitivity and specificity.

Repeatability (sometimes also referred to as precision) is the ability of a test to give consistent results in repeated tests. Repeatability is the converse of variability.

Accuracy is the ability of a test to give a true measure of the item being tested. Accuracy and repeatability are not the same thing. A test can be repeatable without being accurate, but it cannot be accurate without being repeatable. Accuracy has two components, sensitivity and specificity.

Sensitivity is the ability of a test to give a positive result when the animal is diseased. It is measured as the proportion of animals with the disease that give a positive test result.

Specificity is the ability of a test to give a negative result when the animal is not diseased. It is measured as the proportion of disease-free animals that give a negative test result.

Lack of sensitivity leads to false negative results and lack of specificity leads to false positive results.

It is difficult, however, to accurately assess the sensitivity and specificity of a serological test. In general, the sensitivity of a serological test can be estimated by determining the proportion of positive results in those animals that are positive on microbial culture. However, the specificity of a test cannot generally be assessed by determining the proportion of negative results among animals which are negative on microbial culture. This is not only because some animals negative on culture are in fact infected, but, more importantly, because of the very large number of animals it would be necessary to autopsy and take multiple cultures from to accurately determine anything but a very high proportion of false positive results.

Often, in an attempt to assess sensitivity and specificity, the results of one test are compared with those of another test. This does not establish sensitivity and specificity, but only relative sensitivity and relative specificity. Such comparisons are only of value if the sensitivity and specificity of the standard test are known and they approach 100%.

For any given test, sensitivity and specificity are usually inversely related. Thus if the interpretation of test results is altered to increase the sensitivity (to reduce the number of false negative results), then the specificity decreases (and more false positives will result).

The relationship between sensitivity and specificity can be illustrated by the following table:

			health status	
		diseased	not diseased	total
N. 3	positive	a	b	a+b
test result	negative	С	đ	c+d
	total	a+c	b+đ	a+b+c+d = N

a: diseased animals detected by the test

(true positives)

b: non-diseased animals positive to the test (false positives)

c: diseased animals not detected by the test (false negatives)

d: non-diseased animals negative to the test (true negatives)

N: total population

sensitivity = a/(a+c)specificity = d/(b+d)

prevalence = (a+c)/Napparent prevalence = (a+b)/N

predictive value of a positive result = a/(a+b) predictive value of a negative result = d/(c+d)

From this it can be seen that the apparent prevalence observed in a survey will differ from the true prevalence in accordance with the proportion of false positive and false negative results that occur.

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An additional term has also been introduced with this table. The predictive value of a positive result (sometimes also referred to as the validity of the test) is the proportion of the test-positive animals (reactors) that really have the disease. The predictive value is of limited use in comparing tests or interpreting the results of a field survey since it is greatly affected by control measures directed at the disease in question. Although the sensitivity and specificity of a test may be constant during a disease control program, while the true prevalence of the disease is being reduced it is likely that the incidence of false positive animals in the population will be unchanged by the control program. It follows that the observed prevalence of the disease will be comprised of an increasing proportion of false positive reactors as the program progresses. Under these conditions the predictive value of a positive result declines markedly.

4.4 Screening, Surveying, Monitoring and Surveillance

The following definitions are included for the sake of completing this glossary and in an attempt to introduce some precision in the use of these terms.

Screening refers to the testing of a wide cross-section of a population to detect new cases of a disease. The test used usually does not aim at establishing a definitive diagnosis, and so the specificity of the test is not of great importance, and can be compromised for the sake of achieving high sensitivity. The test is usually cheap and easily performed.

The term 'screening test' is also used to refer to a test applied to all samples as a means of cost saving; the negatives are treated as disease free, while the positives undergo a more expensive and/or complex test as a definitive criterion.

 $\underline{\text{Surveying}}$ refers to the testing of a selected sample of a population to determine the prevalence of disease within that population.

Surveillance is the continuous observation of a population aimed at early case—finding for disease control purposes. It generally involves the testing of some section of the population that is readily accessible, e.g. abattoir surveillance or milk ring testing for brucellosis. While the results of disease surveillance may indicate trends in the disease status of a population, they cannot generally be taken as absolute measures of the incidence or prevalence of the disease in the population as a whole unless the surveillance is based on random sampling.

Monitoring is an on-going testing program aimed at the early detection of changes in the prevalence of disease which in turn might indicate a change in the incidence of that disease. Monitoring generally carries the implication of not being accompanied by control measures when positives are detected, but may stimulate control action where monitoring reveals an increasing prevalence.

Table 1 : Detecting the Presence of a Disease

Tables 1(a), 1(b) and 1(c) give 90%, 95% and 99% confidence levels respectively.

These tables may be used in two ways:

- (i) To determine the size of the sample (n) that must be tested to have a given confidence (d) of determining whether a disease is present at a minimum prevalence (d/N) in a population of (N) animals.
- Use the table for the confidence level desired.
- Choose the column corresponding to the percentage of infected animals to be tested against.
- Run down the column to the row that is equal to or greater than the population size to find the required sample size.
- (ii) Having tested a random proportion (n/N) of animals in a population of size (N) and found no positives, the upper limit to the number of positives (d) that could be present can be determined.
- . Use the table for the confidence level desired.
- Choose the column corresponding to the proportion of the population sampled.
- Read off the upper limit to the possible number of positives from the row corresponding to the population size.

Other values

For values not in the table, either interpolation or the following approximation can be used.

If N is the population size,

d is the number of positives in the population,

n is the number sampled

and α is the desired confidence level (that is, the probability of finding at least one positive in the sample)

for (i)
$$n \approx (1 - (1-\alpha)^{1/d})(n - \frac{d}{2}) + 1$$

and (ii)
$$d = (1 - (1-\alpha)^{1/n})(n - \frac{n}{2}) + 1$$

Although not needed here, it is useful to note that

$$\alpha \simeq 1 - \left(1 - \frac{d}{N - (n-1)/2}\right)^n$$

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(i) SAMPLE SIZE REQUIRED FOR DETECTING DISEASE

(ii) CONFIDENCE LIMITS FOR NUMBER OF POSITIVES

	(i)	per	centage	of d	lisease O	d anim	als in	popu	lation	(d/N)		
	(11)	per	centage	samp	oled an	d foun	d clea	n (n/1	%)			
population size (N)	50%	40%	30€ -	251	20%	15%	10%	51	21	18	0.5%	0.1
10	3	4	5	6	7	8	9	10	10			
20	4	5	6	7	ġ	11	14	18		10	10	10
30	4	5	6	8	9	12	16	24	20	20	20	20
40	4	5	6	8	10	12	17	27	30	30	30	30
50	4	5	7	8	10	13	18		38	40	40	41
60	4	5	7	8	10	13	19	30	45	50	50	5
70	14	5	7	. 8 .	10	13	19	32	52	59	60	. 60
80	4	5	'n	8	10	13	20	34	57	68	70	70
90	4	5	ż	8	10	14		35	61	76	80	86
100	4	5	7	8	10	14	20	3.6	65	84	90	9
120	4	5	7	. 8	10	14	20	(37)	.69	91	100	10
140	14	5	ż	8	10		20	38	74	103	118	12
160	14	5	ż	8	10	14	21	39	· 78	113	135	140
180	14	5	7			14	21	40	62	122	152	160
200	1	5	. ,	8	.11	14	21	-40	85	130	167	180
250	1	5	ź	8	11	14	21	41	87	137	180	200
300	1	5		8	11	14	21	42	92	151	211	250
350	11	5	7	8	11	14	22	42 .	95	161	236	300
400	1	2	7	8	11	14	22	43	-98	169	256	350
450	1	5	7	8	11	14	22 .	43	100	175	274	400
500	1	5	7	8	11	14	22	43	101	180	288	448
600	1:	5	7	8	. 11	14	22	43	102	184	301	
700		5	7	8	11	15	22	44	104	191	321	568
800	4	5	7	8	11	15	22	44	106	196	337	675
900	1	5	. 7	8	11	15	22	44	107	200	350	756
1000	4	5	7	8	11	15	22	44	108	203	360	831
1200	4	5	7	8	11	15	22	44	108	205	369	900
1400	4	5	7	8	11	15	22	45	109	209	382	1024
1600	4	5	7	8	11	15	22	45	110	212	392	1130
	4	5	7	8	11	15	22	45	111	214		1221
1800	4	5	7	8	11	15	22	45	111	216		1221
2000	4	5	7	8	11	15	22	45	111	217		1368
3000	4	5	7	8	11	15	22	45	112	221	426	
4000	4	5	7	8	11	15	22	45	113	221	434	1607
5000	4	5	7	8	11	15	22	45	113	224		1750
6000	4	5	7	8	11	15	22	45	113	224	439	1845
7000 .	4	5	7	8	11	15	22	45	114			1912
B000	4	5	7	8	11	15	22	45	114	226		1962
9000	4	5	7	9	11	15	22	45		226		2000
0000	4	\$	7	9	11	15	22	45	114 114	227		2031
ec.	4	5	7	8	11	15	22	43	114	227	449	2056

The table gives:

- (i) the sample size (n) required to be 90% certain of including at least one positive if the disease is present at the specified level
- (ii) the upper limit to the number (d) of diseased animals in a population given that the specified proportion were tested and found to be negative.

Examples:

- (i) Expected proportion of positives is 26. The population size is 480 - use 500. From the table, a sample of 102 is required to be 90% certain of detecting at least one positive.
- (ii) For a population of 1000, a sample of 10% were all found to be negative. From the table, the 90% confidence limit for the number of positives is 22.

	(i)	perc	entage	of d	iseased	anima	ls in p	popul	ation	(d/n)	•	
	(ii)	perc	entage	samp?	OR Led and	found	clean	(n/N)			
population												
size (N)	50€	40%	30€	25%	20%	15%	10%	5€	24	11	0.5%	0.1%
10	4	5	6	7	8	10	10	10	10	10	10	10
20	4	6	7	9	10	12	16	19	20	20	20	20
30	4	6	8	9	11	14	19	26	30	30	30	30
40	5	6	6	10	12	15	21	31	40	40	40	40
. 50	5	6	8	10	12	16	22	35	48	50	50	50
60	5	6	8	10	12	16	23	38	55	60	60	60
70	5	6	8	10	13	17	24	40	62	70	70	70
80	5	6	8	10	13	17	24	42	68	79	80	80
90	5	6	8	10	13	17	25	43	73	87	90	90
100	5	6	9	10	13	17	25	45	78	96	100	100
120	5	6	9	10	13	18	26	47	86	111	120	120
140	5	6	9	11	13	18	26	48	92		. 139	140
160	5	6	9	11	13	18		49	97	136	157	160
180	5	6	9	11	13	18	27	50	101	146	174	- 180
200	5	6	9	11	13	18		·51 ·	105		.190	200
250	5	6	9	11	14	18	27	53	112	175	228	250
300	5	6	9	11	14	18	28 .	.54	117	189	260	300
350	5	6	9	11	14	18	28	54	121	201	287	350
400	5	6	. 9	11	14	19	28	55	.124	. 211	311	400
450	5	6	9	11	14	19	28	55	127	218	331	450
500	5	6	9	11	14	19	26	56	129	225	. 349	500
600	5	6	9	11 -	14	19	28	56	132	235	379	597
700	5	`6	. 9	11.	14	19	28	57	134	243	402	691
800	5	6,	9	11	14	19	26 .	57	136	249	421	782
900	5	6	9	11	14	19	28	57	137	254	. 437	868
1000	5	6	9	11	14	19	29	57	138	258	450	950
1200	5	6	9	11	14	19	29	57	140	264	471	1102
1400	5	6	9	11	14	19	29	58	141	269	487	1236
1600	5	6	9	11	14	19	29	58	142	272	499	1354
1800	5	6	9	11	14	19	29	58	143	275.	509	1459
2000	5	6	9	11	14	19	29	58	143	277	517	1553
3000	5	6	9	11	14	19	29	58	145	284	542	1895
4000	5	6	9	11	14	19	29	58	146	288	556	2108
5000	5	6	9	11	14	19	29	59	147	290	564	2253
6000	5	6	9	11	14	19	29	59	147	291	569	2358
7000	5	6 ·	9	11	14	19 -	29	59	147	292	573	2437
8000	5	6	9	11	14	19	29	59	147	293	576	2498
9000	-5	6	9	11	14	19	29	59	148	294	579	2548
10000	5	6	9	11	14	19	29	59	148	294	581	2588
a.	5	6	9	11	14	19	29	59	149	299	598	2995

The table gives:

- (i) the sample size (n) required to be 95% certain of including at least one positive if the disease is present at the specified level
- (ii) the upper limit to the number (d) of diseased animals in a population given that the specified proportion were tested and found to be negative.

Examples:

- (i) Expected proportion of positives is 2%.

 The population size is 480 use 500.

 From the table, a sample of 129 is required to be 95% certain of detecting at least one positive.
- (ii) For a population of 1000, a sample of 10% were all found to be negative. From the table, the 95% confidence limit for the number of positives is 29.

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Examples:

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2548 2588 581

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40 50

421 437

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- SAMPLE SIZE REQUIRED FOR DETECTING DISEASE (i)
- (ii) CONFIDENCE LIMITS FOR NUMBER OF POSITIVES

		(i)		centag		U	x				(ã/N)		
popul;		'	, per	centag	e samp	red an	d foun	d clea	n (n/l	····			
Size	(N)	50 t	40%	301	25%	20%	151	101	5%	2€	16	0.5%	0.1
10		5	6	7	10	10	10	10	10	10	10	10	10
20		6	8	10	11	13	15	18	20	20	20	20	20
30		6	8	11	13	15	19	23	30	30	30	30	30
40		7	8	11	13	16	21	27	36	40	40	40	40
50		7	9	12	14	17	22	29	42	50	50	50	50
60		7	9	12	14	18	23	31	47	60	60	60	60
70		7	9	12	15	18	24	33	51	68	70	70	70
80		7	9	12	15	19	24	34	54	76	80	80	80
90		7	9	12	15	19	25	35	57	83	90	90	90
100		7	9	13	15	19	25	36	59	90	100	100	100
120		7	9	13	15	19	26	37	63	102	118	120	120
140		7	9	13	16	20	26	38	67	113	135	140	140
160		7	. 9	13	16	20	26	39	69	122	151	160	160
18Q		7	9	13	16	20	27	39	71	129	166	179	180
200		7	9	.13	16	20	27	40	73	136	180	198	200
250		7	9	13	16	20	27	40	76	150	210	244	250
300		7	9	13	16	20	27	41	78	160	235	286	300
		7	9	13	16	21	28	42	80	168	256	325	
400		7	9	13	16	21	28	42	81	174	273	360	350
450		7	9	13	16	21	28	42	82	179	288	392	400
500		7	9	13	16	21	28	42	83	183	300	421	450 500
600		7	9	13	16	21	28	43	84	190	321	470	600
700	•	7	9	13	16	21	28	43	85	195	336	512	700
800		.7	9	13	16	21	28	43	85	199	349	546	798
900		7	9	13	16	21	28	43	86	202	359	576	895
1000		7	9	13	16	21	28	43	86	204	368	601	990
1200		7	9	13	16	21	28	43	87	208	381	642	
1400		7	9	13	16	21	29	44	87	211	391	674	1175
1600		7	9	13	16	21	29	44	88	213	399	699	1348
1800		7	9	13	16	21	29	44	88	215	405		1510
2000		7	9	13	16	21	29	44	88	216	410		1661
3000		7	9	13	16	21	29	44	89	220	425	737	1800
4000	i	7	10	13	16	21	29	44	89	222	433	792	2353
5000		7	10	13	16	21	29	44	89	223	433	821	2735
6000		7	10	13	16	21	29	44	90	223	442	840	3009
7000		7	10	13	16	21	29	44	90	225	444	852	3214
8000	1	7	10	13	16	21	29	44	90	225		861	3373
9000	1	7	10	13	16	21	29	44	90	226	446	668	3500
0000	- 1	7	10	13	16	21	29	44	90	226	447	674	3604
· ec	Į.	7	10	13	16	21	29	44	90	£20	448	878	3689

The table gives:

- (i) the sample size (n) required to be 99% certain of including at least one positive if the disease is present at the specified level
- (ii) the upper limit to the number (d) of diseased animals in a population given that the specified proportion were tested and found to be negative.

Examples:

- Expected proportion of positives is 2%.

 The population size is 480 use 500.

 From the table, a sample of 183 is required to be 99% certain of detecting at least one positive. (i)
- (ii) For a population of 1000, a sample of 10% were all found to be negative. From the table, the 99% confidence limit for the number of positives is 43.

Table 2: Chances of Detecting Positives With Various Intensities of Monitoring

These tables show the effect of different levels of monitoring on the chance of detecting infection that is present at a low level.

Tabulated is the probability of finding at least one positive, given that we are sampling at one of 5 levels (20%, 30%, 40%, 50%, 60%) for populations with a size from 10 to 100, and containing 1 to 8 positives. Under these conditions, with population size greater than 100, the probabilities quickly reach their asymptotic limit for large populations, and this is also given.

Other values can easily be calculated from the approximation mentioned in the notes to Table 1.

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at least one rels (20%, 30%, 10 to 100, and with population y reach their o given.

he approximation

TABLE 2: THE CHANCES OF DETECTING A SHALL RUNGER OF POSITIVES

These tables give the probablility of detecting at least one positive for different sampling intensites and numbers of positives in the population.

TABLE 2(a):

201 SAMPLING

Population Size	number sampled	1	numbe 2	r of po	Eilives 4	in the	popula	tion	•
10 20 30 40 50 60 70 80 90	2 4 6 8 10 12 14 16 18 20	0.200 0.200 0.200	0.363 0.362 0.362 0.362	0.494 0.493 0.492 0.452	G.624 G.612 G.607 G.603 G.601 G.599 G.596 G.597 G.597	0.702 8.694 6.689 8.686 0.686 8.683 6.682	0.753 0.773 0.764 6.758 0.755 0.752 0.751 0.749	0.852 G.630 G.615 G.805 G.807 G.804 G.803	0.576 0.891 0.876 0.857 0.853 0.850 0.850 0.846 0.846 0.846

TABLE 2(b):

304 EAMPTING

population size	number sampled	1	numbe 2	c of p	ositive:	in the	popul.	tion 7	
10 20 30 40 50 60 70 80 90	.3 6 9 12 15 16 21 24 27 30	0.300 0.300 0.300 0.300 0.300 0.300	0.533 0.521 0.517 0.515 0.514 0.514 0.513 0.513 0.512 0.512	0.661 0.666 0.665 0.663 0.663 0.662	0.776 0.773 0.770 0.769 0.768 0.767	0.871 -6.857 -0.851 -0.847 -0.844 -0.842 -0.841 -0.840	0.923 0.909 0.902 0.898 0.895 0.893 0.893	0.956 0.943 0.936 0.933 0.930 0.926 0.927	0.97 0.96 0.95 0.95 0.95

TABLE 2(c):

406 SAMPI THE

Population	number	1	numbe	r of po	citives	in the	popul.			
Size	sampled	7	2 .	3	4	\$. 4	7		
10	4	0.400	0.667	0.633	0.929	C.\$76				
20		E.400	0.653		0.898	C.545			6.994	
. 30	12	0.400		0.300	0.886			0.990	0.994	
40	16	9.400	0 646	0.775	0.500	0.946			C.953	
50	20	0.400		0.755	0.844			0.961	0.950	
60	24				0.581		0.963	0.960	0.549	
70	28	6.400		0.751		G.931	C. 961	0.976	0.916	
80		0.400	0.643	0.790	0.878	8.530	0.960	0.977	0.987	
90	32	0.400	0.643	0.789	0.277		0.959	0.577	0.967	
	36	0.400	0.643	0.789	0.876		0.959			
100	40	0.400	0.642	0.788	0.676				G. 987	
«	•	0.460	0.640		G. 570			0.576	0.966	

TABLE 2(d):

SOL SAMPLING

population gize	number sampled	.1	numbe 2	1 of po	eitives 4	in the	popula 6	tion 7	•
10 20 30 40 50 60 70 80 90 100	\$ 10 15 20 25 30 35 40 45 50 45	0.500 0.500 0.500 0.500 0.500 0.500 0.500 0.500 0.500 0.500	0.763 0.759	0.917 0.295 0.865 0.865 0.863 9.841 0.680 0.879 0.879	0.976 0.957 0.950 0.947 0.945 0.944 0.943 0.942 0.942 0.942	0.984 6.979 0.976 6.975 0.974 6.573	0.994 0.992 0.990 0.989	0.994 0.994 6.994 0.994 0.954	0.994 0.994 0.994 0.994 0.994

TABLE 2(e):

601 SAMPLING

population size	pumber sampled	1	numbe	r of po	sitives	in the	popula	tion	
						•	•	7	
10	۱ ،	0.600	0.867	0.063					
20	12			0.967	0. 374	0. 994	0.994	0.994	0.994
30		0.600		. 0.951 .	0.986	0.994	0.954	0.994	0.994
	18	0.600	0.848	0.246	0.982	0.234	0.994		
40	24	0.600	C. 846	0.943	0.980			0.994	0.394
50	30	6.600				0.993	C. 994	0.954	0.994
			C. 845	0.542	C. 975	0.993	0.954	0.994	0.994
60	36	0.600	0.644	0.941	0. 57E	0.912	0.994		
70	42	0.600	0.843	0.940				0.994	0.954
80	46	1			0.578	0.952	0.954	0.99%	0.994
		0.600	C.843	C. \$40	C.977	0.952	0.994	0.994	0.994
90	54	0.606	0.643	0.535	C. 577	0.951	0.954		
100	60	0.600	0.842				U. 374	0.994	0.994
•				C. 939	C- 577	0.991	0.954	0.954	0.994
	•	0.600	0.540	G. 536	0.574	G. 990	0.996	0.596	0.995

Example

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A 40% sample from a herd of 26 animals would have a 98% chance of including at least one positive if 6 were present in the herd.

Table 3: Probability of Failure to Detect Diseased Animals

The table gives the probability of failure to detect diseased animals from an 'infinite' population with the specified proportion of positives in the population.

prevalence	5	10	number 25	of anim	als in 75	sample 100	tested 200	250	500
1%	0.951	0.904	0.770	0.605					
2%	0.904		0.778	0.605	0.471	0.366	0.134	0.081	0.007
3%		0.817	0.603	0.364	0.220	0.133	0.018	0.006	0.000
48	0.859	0.737	0.467	0.218	0.102	0.048	0.002	0.000	
	0.815	0.665	0.360	0.130	0.047	0.017	0.000		
5%	0.774	0.599	•	0.077	·· 0.021	0.006	0.000		٠,
6%	0.734	0.539	0.213	0.045	0.010	0.002	0.000		
7%	0.696	0.484	0.163	0.027	0.004	0.001	0.000		
88	0.659	0.434	0.124	0.015	0.002	0.000			
98	0.624	0.389	Ò.095	0.009	0.001	0.000			
10%	0.590	0.349	0.072	0.005	0.000	******			
12%	0.528	0.279	0.041	0.002	0.000	•			
14%	0.470	0.221	0.023	0.001	0.000				
16%	0.418	0.175	0.013	0.000	0.000				
18%	0.371	0.137	0.007	0.000					
20%	0.328	0.107	0.004	0.000				J.	
248	0.254	0.064	0.001	0.000					
28%	0.193	0.037	0.000	0.000					
32%	0.145	0.037							
36%	0.145		0.000						
40%		0.012	0.000			•			
50%	0.078	0.006	0.000						
60%	0.031 0.010	0.001	0.000						

While this table is similar to Table 2 in that it shows the effect of sample size on the probability of detecting at least one diseased animal, it approaches the problem differently.

The table assumes a specified number of samples (n) taken from an infinite population with a proportion (θ) of positives. The probability that we fail to detect any positives in the sample is simply:

 $(1 - \theta)^n$

and it is this function that is tabulated.

Example:

Tests of a series of random samples of 25 animals from a large population in which 10% of animals are positive would fail to detect any positives in 7% of such sample groups.

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Table 4: Sample Size for Estimation of Disease Prevalence

The table gives the approximate sample size required to estimate a prevalence in a large population with the desired fixed width confidence limits.

	level of confidence								
expected prevalence	90% desired accuracy 10 5 1			95% desired accuracy 10 5 1			99% desired accuracy		
10% 20% 30% 40% 50% 60% 70%	24 43 57 65 68 65 57 43 24	97 173 227 260 271 260 227 173 97	2435 4329 5682 6494 6764 6494 5682 4329 2435	35 61 81 92 96 92 81 61 35	138 246 323 369 384 369 323 246 138	3457 6147 8067 9220 9604 9220 8067 6147 3457	60 106 139 159 166 159 139 106	557 637 663 637 557 425	5971 10616 13933 15923 16587 15923 13933 10616 5971

The table assumes a knowledge of the approximate result. If in doubt, either use the 0.5 figure, or use the 0.2 figure, but take additional samples if necessary.

When sampling from a finite population of size N, an adjustment to account for this can be made by calculating the sample size n_∞ above and calculating

$$\frac{1}{n} = \frac{1}{n_{cc}} + \frac{1}{N}$$

to give n, the approximate sample size required.

The table is based on the normal approximation to the binomial distribution and Appendix A.2 gives further details.

Choose the desired confidence width, and estimate the values of N that correspond to this width at both p and 1-p, where p is the expected proportion. Use the larger of the two. If the population is not large, the same correction can be made as above.

Example:

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We want to estimate the prevalence of a disease in a herd of 1127 animals to within 5% at the 95% confidence level. We expect that the prevalence would be about 40%.

From the table we see that 369 animals would need to be sampled from a large population, and we correct this for the 'finite population' by calculating

Thus testing of 278 animals would be sufficient.

These graphs give the width of the upper and lower confidence limits for use in estimating disease prevalence from a <u>simple random</u> survey. The confidence limits have been calculated so that the tails are of equal probability. Thus the graphs can be used to find either the 90%, 95% or 99% two-sided limits or the 95%, 97.5% or 99.5% one-sided confidence limits.

- For a sample of size n, in which a proportion p were found to be positive, calculate q = 1-p, the proportion negative
- . The upper limit to the prevalence estimate is found by reading off the graph for the appropriate p and n, and adding this amount to the estimate p
- The lower limit is found by reading off the graph for the appropriate q and n, and subtracting the amount from the estimate p.

This table has been drawn up for use in estimating prevalence in a very large population. For a small population, the width of the confidence intervals should be multiplied by a finite correction factor $\sqrt{1-f}$, where f is the proportion of the population sampled:

Proportion sampled (f) 0 .1 .2 .3 .4 .5 .6 .7 .8 .9 1.0 Correction factor ($\sqrt{1-f}$) 1 .95 .90 .84 .78 .71 .64 .55 .45 .32 .0

confidence interval (w)

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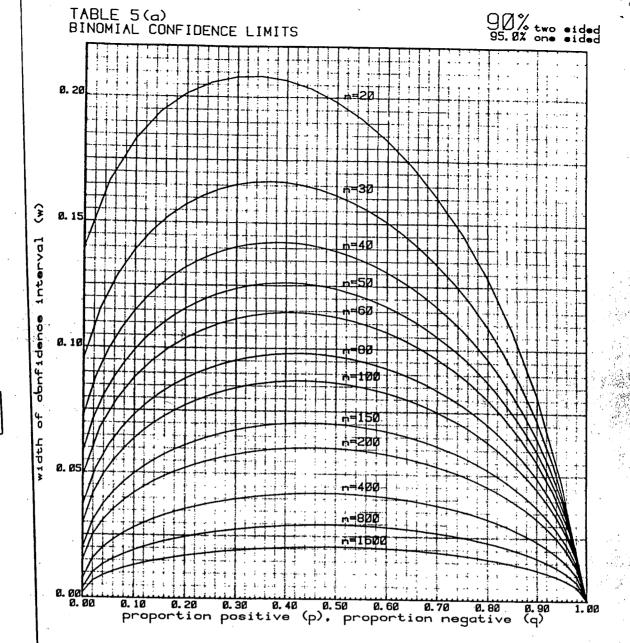
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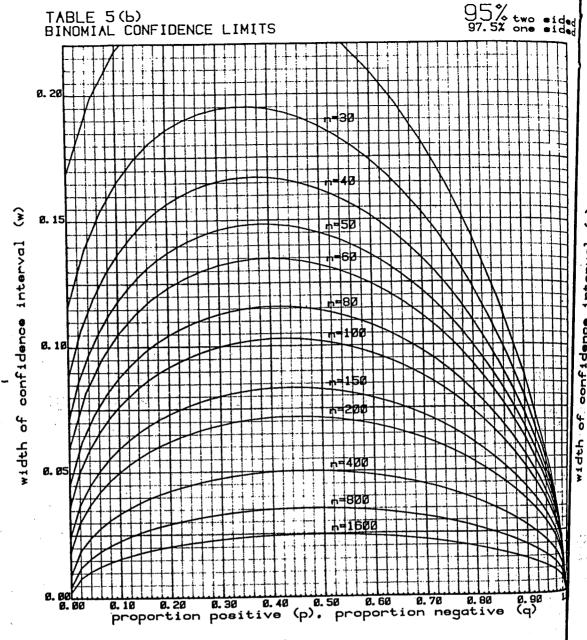
The table gives the width (w) of two sided 90% confidence limits for a prevalence given an observed proportion (p) of positives with different sample sizes (n).

Examples

In a sample of 60 animals, 12 were found to be positive Calculate p = 12/60 = .2 and q = 1 - p = .8

Read off
upper width of 0.104 at p
and lower width of 0.080 at q

90% confidence limits for the prevalence are (0.120 - 0.304)



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99% 001

The table gives the width (w) of two sided 95% confidence limits for a prevalence given an observed proportion (p) of positives with different sample sizes (n).

Example:

In a sample of 60 animals, 12 were found to be positive Calculate p = 12/60 = .2 and q = 1 - p = .8Read off upper width of 0.123 at p . 2t./23t.323 and lower width of 0.092 at q . 2t./23t.323

95% confidence limits for the prevalence are (0.108 - 0.323)

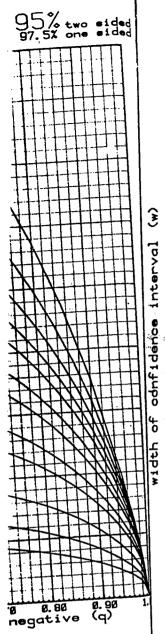
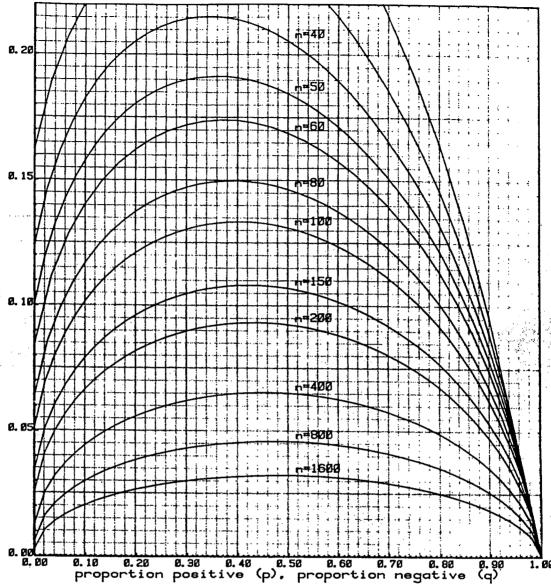


TABLE 5'(e)
BINOMIAL CONFIDENCE LIMITS

99.5% two eided



confidence rtion (p)

positive = .8

Ø. 108 - Ø. 323)

The table gives the width (w) of two sided 99% confidence limits for a prevalence given an observed proportion (p) of positives with different sample sizes (n).

Examples

In a sample of 60 animals, 12 were found to be positive

Calculate p = 12/60 = .2 and q = 1 - p = .8

Read off

upper width of 0.162 at p and lower width of 0.113 at q

99% confidence limits for the prevalence are (0.087 - 0.362)

Table 6: Random Numbers

The table consists of sets of two-digit random numbers. It can be used in selecting a random sample from any population of known size.

To select a sample of a required size, start at any point in the table and move systematically down columns and along rows until a sample of the required size is obtained. Where a number is duplicated in the group selected it should be ignored and the next random number in the sequence used. Similarly if a number falls outside the range of the population size it should be skipped over and next random number used. This does not affect the randomness of the sample.

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73 82 35 07

49 87 55 07

33 25 03 79

> 33 51

Examples:

Control of the Contro

- i) To select a random sample of 10 from a herd of 40
 - . Number the animals 1 to 40
 - . Start at any point in the random number table
 - . Work down the column writing down each number that is from 1 to 40 but rejecting repetitions until you have ten numbers.

To avoid 'wasting' random numbers, subtract 40 from any numbers over 40 and use the result if it is 40 or less. But if the result is again over 40, do not repeat this process. The numbers would then only go from 1 to 19 and there would be no chance of selecting 20 to 40.

In the sequence of random numbers below, the ten animals chosen are underlined. Note that both 6 and 13 were duplicated in the list.

random number: 98 05 89 80 23 64 53 60 75 84 06 88 06 11 13 16 81 subtract 40: 58 49 40 24 13 20 35 44 48

The sample would comprise animals 5, 6, 11, 13, 16, 20, 23, 24, 35 and 40.

- ii) To sample a tenth of the sheep on a property where these are in three mobs of 357, 117 and 310 respectively:
 - . Using the method of (i), random samples of 36, 12 and 31 respectively may be selected from the three mobs to give a stratified sample
 - . Alternatively use pairs of two-digit random numbers to create a number between 0 and 999 by ignoring the fourth digit.

For random numbers:

1-357 - first paddock, sheep 1-357 401-517 - second paddock, sheep 1-117 601-910 - third paddock, sheep 1-310

Ignore any other numbers.

- iii) To sample an eighth of the items from a continuous production process:
 - . Start at any point in the random number table
 - If the last digit in the two-digit random number is 0 or 9 ignore it, and use the next random number
 - . Sample the item if the last digit is 2.

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A.1 Testing for the Presence of a Disease

Suppose that we are sampling a population to test that there are no positives in the population.

Let

N be the population size,

d be the number of diseased animals in the population

n be the number of animals sampled

and β be the probability that there are no positives in the sample.

Either from first principles, or from the hypergeometric distribution, these four variables are related by

$$\beta = \frac{N-d}{N} \cdot \frac{N-d+1}{N-1} \cdot \cdot \cdot \cdot \frac{N-d-n+1}{N-n+1}$$
 (1)

which may be rewritten as

$$\beta = \frac{(N-d)! (N-n)!}{N! (N-d-n)!}$$
 (2)

Equation (1) simply states that the probability that there are no positives in the sample is equal to the probability a positive is not the first animal sampled times the probability that a positive is not the second animal sampled, and so on, to the probability that a positive is not the nth animal sampled.

In order to answer the question 'How many to sample?', we take the N and d of interest and successively multiply the terms in (1) until we get a product less than the desired level. If we choose this value of n as our sample size, the chances of finding at least one of the d positives will be $1-\beta$, the confidence level that we want.

It is more tedious to answer—the question 'If—I find no positives in a sample what is an upper limit to the number of positives?' Simplistically trial and error could be used to solve (1) for d given N, n and β . Luckily there is a very good approximation available. Each term in the numerator and denominator of (1) can be approximated by the 'middle' term of the product to give:

$$\beta \simeq \left(\frac{N-d-(n-1)/2}{N-(n-1)/2}\right)^n = \left(1-\frac{d}{N-(n-1)/2}\right)^n$$

By taking the nth root, we find that d is given by:

$$d \approx (1-\beta)^{1/n})(n-\frac{n-1}{2})$$

and this is basica/lly the approximation referred to in Table 1.

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If we look at equation (2) we see that d and n can be interchanged without changing the formula. This is why Table 1 can be used to answer both questions. It also means that the same form of approximation can be used to quickly obtain the sample size:

$$n \approx (1-\beta^{1/d})(N-\frac{d-1}{2})$$

As the population size increases but θ = d/N, the proportion of diseased animals, remains constant, then equation (1) becomes

$$\theta = (1-\beta)^n \tag{3}$$

(This is equivalent to the binominal approximation to the hypergeometric distribution.)

Solving (3) for n gives:

$$n = \log \beta / \log(1-\theta)$$

as the limit to the sample size required, and

$$\theta = 1 - g 1/n$$

as the upper limit to the proportion of diseased animals in the population if no positives are found in a sample from a very large population.

A.2 Estimating a Proportion:

This section considers the problems concerning the estimation of the actual level of disease, rather than simply determining its absence or presence.

Again we shall consider a population of size N with $d=N\theta$ diseased animals. We shall take a sample of size n and look at the (random) number X of diseased animals in the sample.

The statistical distribution that describes this form of sampling is the hypergeometric distribution. From simple combinational arguments we can show that the probability that we get \mathbf{x} positives in the sample is

Prob
$$\{x=x\} = {d \choose x} {N-d \choose n-x} {N \choose n}$$

The mean of X is $n\theta$ and the variance is $n\theta\,(1-\theta)\frac{N-n}{N-1}$.

If the population size is large, the binomial distribution can be used to approximate the hypergeometric distribution to give

Prob
$$\{X=x\} = \binom{n}{x} \theta^{x} (1-\theta)^{n-x}$$

X has mean and variance of $n\theta$ and $n\theta$ (1- θ) respectively.

We want to answer three questions:

- i) what is an estimate of θ ?
- ii) what are confidence limits for θ ?
- iii) how big a sample should we take to get specified confidence limits? (which should have been asked first).

i) Estimating the proportion

Regardless of the population size, we shall use p=x/n as an estimate of the proportion of diseased animals.

ii) Finding confidence limits for a proportion

Initially we shall assume that the sample is from an infinite population and later give an approximation to take into account the population size.

When determining confidence limits, we are looking for values of θ for which the observed value is 'likely'. Put another way, if the probability of observing the same or worse result for a particular value of θ is small, then that value of θ is not included in the confidence limits. This reasoning leads to solving the equation

$$\beta = \sum_{i=0}^{x} {n \choose i} \quad \theta^{i} (1-\theta)^{n-i} \qquad \text{for } \theta.$$

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There is no elegant easy alternative to using a systematic trial and error approach.

Table 5 provides these confidence limits.

The effect of the finite population size is to reduce the variance by the fraction (N-n)/(N-1). We should then expect that the width of the confidence limits would be reduced by a factor of

$$\sqrt{\frac{N-n}{N-1}}$$
 or approximately $\sqrt{(1-\frac{n}{N})}$.

This approximation turns out to be quite good for middle sized values of θ , but it over estimates the reduction for lower limits near $\theta = 0$, and upper limits near $\theta = 1$ (because the variable cannot go outside the range of 0 and 1).

For large values of n (say greater than 50), the normal approximation to the binomial distribution holds fairly well at the tails of the distribution. If v is the corresponding normal percentage point, then approximate confidence limits are given by

$$p + (v \sqrt{\frac{p(1-p)}{n}} (1 - \frac{n}{N}) + \frac{1}{2n})$$

iii) Approximate sample size required

Before doing the sampling, it is worthwhile estimating the sample size required to give the desired width of confidence limits, say +w.

Using the normal approximation mentioned above, this requirement means that, for an infinite population,

$$w = v \sqrt{\theta(1-\theta)/n}$$

By solving this for n, we obtain

$$n_m = (v/w)^2 \theta (1-\theta)$$

and it is this function that is given in Table 4.

For a finite population, the requirement implies that

$$w = v \sqrt{\frac{\theta(1-\theta)}{n} (1-\frac{n}{N})} = v \sqrt{\theta(1-\theta)(\frac{1}{n}-\frac{1}{N})}$$

By squaring and rearranging we get

$$\frac{1}{n} = \frac{1}{N} + \left(\frac{w}{v}\right)^2 \frac{1}{\theta(1-\theta)} = \frac{1}{N} + \frac{1}{n}$$

A.3 Estimating Population Size

Sometimes we do not know the population size, but rather are wanting to estimate it. Typical cases would concern feral animals or where mustering is difficult.

One method is to use a capture-recapture sampling scheme.

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Suppose that an initial sample of d animals are captured, marked in some way and released. After a time suitable to allow for mixing of the population, but which would preclude many deaths/births, another sample of n (the recapture) is done. X is the number of the original sample recaptured.

An estimation of the population size is given by N = $d_{\mathbf{x}}^{\mathbf{n}}$

- (i) estimate $N = d^{\frac{n}{n}}$
- (ii) calculate p = d/N, q=1-p, f=n/N
- (iii) calculate upper and lower limits for p (from Table 5) after adjusting the width by the finite population correction factor (/1-f)
- (iv) estimate upper and lower estimates using d/p.

Often only an upper limit for N is required. In this case only the lower one-sided limit for p needs to be calculated.

Example 1:

At the first round of testing of a herd, 120 animals were mustered. At the second round, 130 animals, which included 110 of those present at the first test, were mustered. How many animals are untested?

We have d=120, n=130 and x=110

- (i) This gives an estimate of N=120 x 130 \div 110 = 141
- (ii) p=.85, q=.15, f=.92, $\sqrt{1-f}$ =.28
- (iii) from the 95% table the lower limit is $.85 (.07 \times .28) = .85 0.0196 = .8304$
- (iv) whence 95% confidence limit for the maximum value of N is 144

Thus: 110 were tested twice

- 10 were presented for first test but not second 20 were presented for second test but not first
 - 4 remain untested.

Example 2:

400 feral pigs are captured, marked and then released. 40 of the original capture are found when another 400 pigs are captured.

We have d=400, n=400, and x=40.

- (i) N=4000
- (ii) $p=.1, q=.9, f=.9, \sqrt{1-f} = .95$
- (iii) upper limit is .1 + (.025 x .95) = .1037 lower limit is .1 (.025 x .95) = .0763
- (iv) 95% limits for N are (3233, 5249).

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A.4 Further Reading

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